



SEQUENCE LISTING

<110> STEINMAN, RALPH A
NUSSENZWEIG, MICHEL C
SWIGGARD, WILLIAM J
JIANG, WANPING

<120> IDENTIFICATION OF DEC, A RECEPTOR WITH
C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND USES
THEREOF

<130> 600-1-081CON

<140> 09/586,704

<141> 2000-06-05

<150> 08/381,528

<151> 1995-01-31

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 65 70 75 80
 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ala Thr Asp Asn Leu Arg
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 Met Phe Ser Cys Asp Ser Thr Val Met Leu Trp Trp Lys Cys Glu His
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 His Ser Leu Tyr Thr Ala Ala Gln Tyr Arg Leu Ala Leu Lys Asp Gly
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 Tyr Ala Val Ala Asn Thr Asn Thr Ser Asp Val Trp Lys Lys Gly Gly
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 Ser Glu Glu Asn Leu Cys Ala Gln Pro Tyr His Glu Ile Tyr Thr Arg
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 Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Gly
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 Glu Thr Trp Tyr His Asp Cys Ile His Asp Glu Asp His Ser Gly Pro
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 Trp Cys Ala Thr Thr Leu Ser Tyr Glu Tyr Asp Gln Lys Trp Gly Ile
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 Cys Leu Leu Pro Glu Ser Gly Cys Glu Gly Asn Trp Glu Lys Asn Glu
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 Gln Ile Gly Ser Cys Tyr Gln Phe Asn Asn Gln Glu Ile Leu Ser Trp
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 Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
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 Ile His Ser Ala Ala Glu Leu Ala Tyr Ile Thr Gly Lys Glu Asp Ile
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 Trp Glu Trp Ser Asp Phe Arg Pro Leu Lys Phe Leu Asn Trp Asp Pro
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 Gly Thr Pro Val Ala Pro Val Ile Gly Gly Ser Ser Cys Ala Arg Met
 305 310 315 320
 Asp Thr Glu Ser Gly Leu Trp Gln Ser Val Ser Cys Glu Ser Gln Gln
 325 330 335
 Pro Tyr Val Cys Lys Lys Pro Leu Asn Asn Thr Leu Glu Leu Pro Asp
 340 345 350
 Val Trp Thr Tyr Thr Asp Thr His Cys His Val Gly Trp Leu Pro Asn
 355 360 365
 Asn Gly Phe Cys Tyr Leu Leu Ala Asn Glu Ser Ser Ser Trp Asp Ala
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		835					840					845			

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Ala	Leu	Ser	Lys	Tyr	Gly	Val	Asn	Trp	Trp	Ile	Gly	Leu	Arg	Glu	Glu	865	870	875
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Gln	Asn	Trp	Asp	Lys	Gly	Lys	Glu	Arg	Ser	Met	Gly	Leu	Asn	Glu	Ser	900	905	910
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Val	Ile	Glu	Lys	Lys	Lys	Asp	Ile	Pro	Lys	Gln	His	Gly	Thr	Cys	Pro	945	950	955
Lys	Gly	Trp	Leu	Tyr	Phe	Asp	Tyr	Lys	Cys	Leu	Leu	Leu	Lys	Ile	Pro	965	970	975
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Glu	Ser	Ser	Phe	Leu	Gly	Asp	Cys	Val	Phe	Ala	Asp	Thr	Ser	Gly	Arg	1205	1210	1215
Trp	Ser	Ser	Thr	Ala	Cys	Glu	Ser	Tyr	Leu	Gln	Gly	Ala	Ile	Cys	Gln	1220	1225	1230
Val	Pro	Thr	Glu	Thr	Arg	Leu	Ser	Gly	Arg	Leu	Glu	Leu	Cys	Ser	Glu	1235	1240	1245
Thr	Ser	Ile	Pro	Trp	Ile	Lys	Phe	Lys	Ser	Asn	Cys	Tyr	Ser	Phe	Ser	1250	1255	1260
Thr	Val	Leu	Glu	Ser	Thr	Ser	Phe	Glu	Ala	Ala	His	Glu	Phe	Cys	Lys	1265	1270	1275
Lys	Lys	Gly	Ser	Asn	Leu	Leu	Thr	Ile	Lys	Asp	Glu	Ala	Glu	Asn	Ser	1285	1290	1295
Phe	Leu	Leu	Glu	Glu	Leu	Leu	Ala	Phe	Arg	Ser	Ser	Val	Gln	Met	Ile			

				1300					1305					1310					
Trp	Leu	Asn	Ala	Gln	Phe	Asp	Gly	Asp	Asn	Glu	Thr	Ile	Lys	Trp	Phe				
		1315						1320					1325						
Asp	Gly	Thr	Pro	Thr	Asp	Gln	Ser	Asn	Trp	Gly	Ile	Arg	Lys	Pro	Glu				
	1330					1335					1340								
Val	Tyr	His	Phe	Lys	Pro	His	Leu	Cys	Val	Ala	Leu	Arg	Ile	Pro	Glu				
1345					1350					1355					1360				
Gly	Val	Trp	Gln	Leu	Ser	Ser	Cys	Gln	Asp	Lys	Lys	Gly	Phe	Ile	Cys				
				1365					1370					1375					
Lys	Met	Glu	Ala	Asp	Ile	His	Thr	Val	Lys	Lys	His	Pro	Gly	Lys	Gly				
		1380						1385					1390						
Pro	Ser	His	Ser	Val	Ile	Pro	Leu	Thr	Val	Ala	Leu	Thr	Leu	Leu	Val				
		1395					1400					1405							
Ile	Leu	Ala	Ile	Ser	Thr	Leu	Ser	Phe	Cys	Met	Tyr	Lys	His	Ser	His				
	1410					1415					1420								
Ile	Ile	Phe	Gly	Arg	Leu	Ala	Gln	Phe	Arg	Asn	Pro	Tyr	Tyr	Pro	Ser				
1425				1430					1435					1440					
Ala	Asn	Phe	Ser	Thr	Val	His	Leu	Glu	Glu	Asn	Ile	Leu	Ile	Ser	Asp				
			1445					1450					1455						
Leu	Glu	Lys	Asn	Asp	Gln														
			1460																

<210> 5

<211> 1457

<212> PRT

<213> homo sapiens

<220>

<223> macrophage mannose receptor

<400> 5

Met	Arg	Leu	Pro	Leu	Leu	Leu	Val	Phe	Ala	Ser	Val	Ile	Pro	Gly	Ala				
1				5				10						15					
Val	Leu	Leu	Leu	Asp	Thr	Arg	Gln	Phe	Leu	Ile	Tyr	Asn	Glu	Asp	His				
			20					25					30						
Lys	Arg	Cys	Val	Asp	Ala	Val	Ser	Pro	Ser	Ala	Val	Gln	Thr	Ala	Ala				
		35					40					45							
Cys	Asn	Gln	Asp	Ala	Glu	Ser	Gln	Lys	Phe	Arg	Trp	Val	Ser	Glu	Ser				
	50					55					60								
Gln	Ile	Met	Ser	Val	Ala	Phe	Lys	Leu	Cys	Leu	Gly	Val	Pro	Ser	Lys				
65				70				75						80					
Thr	Asp	Trp	Val	Ala	Ile	Thr	Leu	Tyr	Ala	Cys	Asp	Ser	Lys	Ser	Glu				
			85					90					95						
Phe	Gln	Lys	Trp	Glu	Cys	Lys	Asn	Asp	Thr	Leu	Leu	Gly	Ile	Lys	Gly				
		100						105					110						
Glu	Asp	Leu	Phe	Phe	Asn	Tyr	Gly	Asn	Arg	Gln	Glu	Lys	Asn	Ile	Met				
	115						120					125							
Leu	Tyr	Lys	Gly	Ser	Gly	Leu	Trp	Ser	Arg	Trp	Lys	Ile	Tyr	Gly	Thr				
	130					135					140								
Thr	Asp	Asn	Leu	Cys	Ser	Arg	Gly	Tyr	Glu	Ala	Met	Tyr	Thr	Leu	Leu				
145				150						155				160					
Gly	Asn	Ala	Asn	Gly	Ala	Thr	Cys	Ala	Phe	Pro	Phe	Lys	Phe	Glu	Asn				
			165					170					175						
Lys	Trp	Tyr	Ala	Asp	Cys	Thr	Ser	Ala	Gly	Arg	Ser	Asp	Gly	Trp	Leu				
		180						185				190							
Trp	Cys	Gly	Thr	Thr	Thr	Asp	Tyr	Asp	Thr	Asp	Lys	Leu	Phe	Gly	Tyr				

		195					200					205			
Cys	Pro	Leu	Lys	Phe	Glu	Gly	Ser	Glu	Ser	Leu	Trp	Asn	Lys	Asp	Pro
	210					215					220				
Leu	Thr	Ser	Val	Ser	Tyr	Gln	Ile	Asn	Ser	Lys	Ser	Ala	Leu	Thr	Trp
225					230					235					240
His	Gln	Ala	Arg	Lys	Ser	Cys	Gln	Gln	Gln	Asn	Ala	Glu	Leu	Leu	Ser
				245						250				255	
Ile	Thr	Glu	Ile	His	Glu	Gln	Thr	Tyr	Leu	Thr	Gly	Leu	Thr	Ser	Ser
			260					265					270		
Leu	Thr	Ser	Gly	Leu	Trp	Ile	Gly	Leu	Asn	Ser	Leu	Ser	Phe	Asn	Ser
		275					280				285				
Gly	Trp	Gln	Trp	Ser	Asp	Arg	Ser	Pro	Phe	Arg	Tyr	Leu	Asn	Trp	Leu
	290					295					300				
Pro	Gly	Ser	Pro	Ser	Ala	Glu	Pro	Gly	Lys	Ser	Cys	Val	Ser	Leu	Asn
305					310					315					320
Pro	Gly	Lys	Asn	Ala	Lys	Trp	Glu	Asn	Leu	Glu	Cys	Val	Gln	Lys	Leu
			325						330					335	
Gly	Tyr	Ile	Cys	Lys	Lys	Gly	Asn	Thr	Thr	Leu	Asn	Ser	Phe	Val	Ile
			340					345					350		
Pro	Ser	Glu	Ser	Asp	Val	Pro	Thr	His	Cys	Pro	Ser	Gln	Trp	Trp	Pro
		355					360					365			
Tyr	Ala	Gly	His	Cys	Tyr	Lys	Ile	His	Arg	Asp	Glu	Lys	Lys	Ile	Gln
	370					375					380				
Arg	Asp	Ala	Leu	Thr	Thr	Cys	Arg	Lys	Glu	Gly	Gly	Asp	Leu	Thr	Ser
385					390					395					400
Ile	His	Thr	Ile	Glu	Glu	Leu	Asp	Phe	Ile	Ile	Ser	Gln	Leu	Gly	Tyr
			405						410					415	
Glu	Pro	Asn	Asp	Glu	Leu	Trp	Ile	Gly	Leu	Asn	Asp	Ile	Lys	Ile	Gln
			420					425					430		
Met	Tyr	Phe	Glu	Trp	Ser	Asp	Gly	Thr	Pro	Val	Thr	Phe	Thr	Lys	Trp
		435					440					445			
Leu	Arg	Gly	Glu	Pro	Ser	His	Glu	Asn	Asn	Arg	Gln	Glu	Asp	Cys	Val
	450					455					460				
Val	Met	Lys	Gly	Lys	Asp	Gly	Tyr	Trp	Ala	Asp	Arg	Gly	Cys	Glu	Trp
465					470					475					480
Pro	Leu	Gly	Tyr	Ile	Cys	Lys	Met	Lys	Ser	Arg	Ser	Gln	Gly	Pro	Glu
				485					490					495	
Ile	Val	Glu	Val	Glu	Lys	Gly	Cys	Arg	Lys	Gly	Trp	Lys	Lys	His	His
			500					505					510		
Phe	Tyr	Cys	Tyr	Met	Ile	Gly	His	Thr	Leu	Ser	Thr	Phe	Ala	Glu	Ala
		515					520					525			
Asn	Gln	Thr	Cys	Asn	Asn	Glu	Asn	Ala	Tyr	Leu	Thr	Thr	Ile	Glu	Asp
	530					535					540				
Arg	Tyr	Glu	Gln	Ala	Phe	Leu	Thr	Ser	Phe	Val	Gly	Leu	Arg	Pro	Glu
545															

Ser	Leu	Cys	Phe	Lys	Leu	Tyr	Ala	Lys	Gly	Lys	His	Glu	Lys	Lys	Thr
			660					665					670		
Trp	Phe	Glu	Ser	Arg	Asp	Phe	Cys	Arg	Ala	Leu	Gly	Gly	Asp	Leu	Ala
		675					680					685			
Ser	Ile	Asn	Asn	Lys	Glu	Glu	Gln	Gln	Thr	Ile	Trp	Arg	Leu	Ile	Thr
	690					695					700				
Ala	Ser	Gly	Ser	Tyr	His	Lys	Leu	Phe	Trp	Leu	Gly	Leu	Thr	Tyr	Gly
705					710					715					720
Ser	Pro	Ser	Glu	Gly	Phe	Thr	Trp	Ser	Asp	Gly	Ser	Pro	Val	Ser	Tyr
				725					730					735	
Glu	Asn	Trp	Ala	Tyr	Gly	Glu	Pro	Asn	Asn	Tyr	Gln	Asn	Val	Glu	Tyr
			740					745					750		
Cys	Gly	Glu	Leu	Lys	Gly	Asp	Pro	Thr	Met	Ser	Trp	Asn	Asp	Ile	Asn
		755					760					765			
Cys	Glu	His	Leu	Asn	Asn	Trp	Ile	Cys	Gln	Ile	Gln	Lys	Gly	Gln	Thr
	770					775					780				
Pro	Lys	Pro	Glu	Pro	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Pro	Pro	Val	Thr
785					790					795					800
Glu	Asp	Gly	Trp	Val	Ile	Tyr	Lys	Asp	Tyr	Gln	Tyr	Tyr	Phe	Ser	Lys
				805					810					815	
Glu	Lys	Glu	Thr	Met	Asp	Asn	Ala	Arg	Ala	Phe	Cys	Lys	Arg	Asn	Phe
			820					825					830		
Gly	Asp	Leu	Val	Ser	Ile	Gln	Ser	Glu	Ser	Glu	Lys	Lys	Phe	Leu	Trp
		835					840					845			
Lys	Tyr	Val	Asn	Arg	Asn	Asp	Ala	Gln	Ser	Ala	Tyr	Phe	Ile	Gly	Leu
	850					855					860				
Leu	Ile	Ser	Leu	Asp	Lys	Lys	Phe	Ala	Trp	Met	Asp	Gly	Ser	Lys	Val
865					870					875					880
Asp	Tyr	Val	Ser	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Glu	Asp
				885					890					895	
Glu	Asn	Cys	Val	Thr	Met	Tyr	Ser	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile
			900					905					910		
Asn	Cys	Gly	Tyr	Pro	Asn	Ala	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser
		915					920					925			
Ile	Asn	Ala	Thr	Thr	Val	Met	Pro	Thr	Met	Pro	Ser	Val	Pro	Ser	Gly
	930					935					940				
Cys	Lys	Glu	Gly	Trp	Asn	Phe	Tyr	Ser	Asn	Lys	Cys	Phe	Lys	Ile	Phe
945					950					955					960
Gly	Phe	Met	Glu	Glu	Glu	Arg	Lys	Asn	Trp	Gln	Glu	Ala	Arg	Lys	Ala
				965					970					975	
Cys	Ile	Gly	Phe	Gly	Gly	Asn	Leu	Val	Ser	Ile	Gln	Asn	Glu	Lys	Glu
			980					985					990		
Gln	Ala	Phe	Leu	Thr	Tyr	His	Met	Lys	Asp	Ser	Thr	Phe	Ser	Ala	Trp
		995					1000						1005		
Thr	Gly	Leu</													

1105 1110 1115 1120
 Thr Tyr Cys Lys Leu His Asn Ser Leu Ile Ala Ser Ile Leu Asp Pro
 1125 1130 1135
 Tyr Ser Asn Ala Phe Ala Trp Leu Gln Met Glu Thr Ser Asn Glu Arg
 1140 1145 1150
 Val Trp Ile Ala Leu Asn Ser Asn Leu Thr Asp Asn Gln Tyr Thr Trp
 1155 1160 1165
 Thr Asp Lys Trp Arg Val Arg Tyr Thr Asn Trp Ala Ala Asp Glu Pro
 1170 1175 1180
 Lys Leu Lys Ser Ala Cys Val Tyr Leu Asp Leu Asp Gly Tyr Trp Lys
 1185 1190 1195 1200
 Thr Ala His Cys Asn Glu Ser Phe Tyr Phe Leu Cys Lys Arg Ser Asp
 1205 1210 1215
 Glu Ile Pro Ala Thr Glu Pro Pro Gln Leu Pro Gly Arg Cys Pro Glu
 1220 1225 1230
 Ser Asp His Thr Ala Trp Glu Ile Pro Phe His Gly His Cys Tyr Tyr
 1235 1240 1245
 Ile Glu Ser Ser Tyr Thr Arg Asn Trp Gly Gln Ala Ser Leu Glu Cys
 1250 1255 1260
 Leu Arg Met Gly Ser Ser Leu Val Ser Ile Glu Ser Ala Ala Glu Ser
 1265 1270 1275 1280
 Ser Phe Leu Ser Tyr Arg Val Glu Pro Leu Lys Ser Lys Thr Asn Phe
 1285 1290 1295
 Trp Ile Gly Leu Phe Arg Asn Val Glu Gly Thr Trp Leu Trp Ile Asn
 1300 1305 1310
 Asn Ser Pro Val Ser Phe Val Asn Trp Asn Thr Gly Asp Pro Ser Gly
 1315 1320 1325
 Glu Arg Asn Asp Cys Val Ala Leu His Ala Ser Ser Gly Phe Trp Ser
 1330 1335 1340
 Asn Ile His Cys Ser Ser Tyr Lys Gly Tyr Ile Cys Lys Arg Pro Lys
 1345 1350 1355 1360
 Ile Ile Asp Ala Lys Pro Thr His Glu Leu Leu Thr Thr Lys Ala Asp
 1365 1370 1375
 Thr Arg Lys Met Asp Pro Ser Lys Pro Ser Ser Asn Val Ala Gly Val
 1380 1385 1390
 Val Ile Ile Val Ile Leu Leu Ile Leu Thr Gly Ala Gly Leu Ala Ala
 1395 1400 1405
 Tyr Phe Phe Tyr Lys Lys Arg Arg Val His Leu Pro Gln Glu Gly Ala
 1410 1415 1420
 Phe Glu Asn Thr Leu Tyr Phe Asn Ser Gln Ser Ser Pro Gly Thr Ser
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 1445 1450 1455
 Ile

<210> 6

<211> 30

<212> PRT

<213> mus musculus

<220>

<223> C terminal DEC-205

<400> 6

Arg Ser His Ile Arg Trp Thr Gly Phe Ser Ser Val Arg Tyr Glu His

<213> homo sapiens

<220>

<221> VARIANT

<222> 1, 3, 4

<223> Xaa at position 1 is Glu or Gln; Xaa at position 3 and 4 are Asp or Asn.

<400> 10

Xaa Pro Xaa Xaa

1

<210> 11

<211> 5

<212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> 1, 2, 4, 5

<223> Xaa at position 1 is aromatic; Xaa at position 2 and 4 are aliphatic; Xaa at position 5 is any of Asp, Asn, Glu, or Gln.

<400> 11

Xaa Xaa Gly Xaa Xaa

1

5

<210> 12

<211> 5

<212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> 2, 4, 5

<223> Xaa at position 5 is aliphatic or aromatic; Xaa at position 4 is aliphatic; Xaa at position 2 is any of Asp, Asn, Glu, or Gln.

<400> 12

Glu Xaa Cys Xaa Xaa

1

5

<210> 13

<211> 19

<212> PRT

<213> mus musculus

<400> 13

Ser Glu Ser Ser Gly Asn Asp Pro Phe Thr Ile Val His Glu Asn Thr

1

5

10

15

Gly Lys Cys